From: Jay Field
To: Eric Blischke/R10/USEPA/US@EPA
Cc: Robert Neely
Subject: Re: LRM
Date: 12/21/2007 10:04 AM

Eric,
thanks for the feedback. I'll try to finish up the growth endpoint discussion this weekend.
Jay

Blischke.Eric@epamail.epa.gov wrote:
> Jay, the first paragraph summarizing the rationale for the inclusion of
> non-site data is right on. I understand that the discussion regarding
> the Hyalella growth endpoint is incomplete but I think including the
> total biomass discussion is good. Based on our conversation the other
> day, I am assuming that you will demonstrating that whether the Hyalella
> growth endpoint or the total biomass endpoint is considered, that by
> using the most sensitive endpoint, you get essentially the same results.
> I would expect that more discussion on the possible use of the total
> biomass endpoint will ensue.
>
> Eric
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>
> Jay Field
> <Jay.Field@noaa.
> gov> To
> Eric Blischke/R10/USEPA/US@EPA,
> 12/20/2007 02:36 Robert Neely
> PM <Robert.Neely@noaa.gov>
> cc
>
> Subject
> LRM
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> Eric,
> is this the type of text you had in mind? I have to leave now, but will
>
> try to complete in the next few days when I can steal some time.
> Have a great holiday.
> Jay
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>
> Inclusion of non-site data in addition to PH data in the derivation of
> individual chemical logistic regression models (LRMs):
>
> Individual chemical logistic regression models for Hyalella azteca (HA)
> growth and survival were developed using the Portland Harbor Round 2
> data (n=233) and data from a national freshwater database (n=401) for
> the HA 28-day growth and survival endpoint. The individual models were
> selected based on their performance with the Portland Harbor data only.
>
> Performance of the individual models was evaluated on the the number of
> false positives (samples with a high probability of toxicity that were
> not toxic). Similarly, the combined P_Max model, which uses the maximum
>
> probability for each sample, was calibrated to the Portland Harbor data
> only. It is not surprising that the individual models derived from the
> larger database performed better than models derived from the Portland
> Harbor data. Based on our experience in developing LRMs, models derived
>
> from a larger database including data from a broad range of chemical
> concentrations and multiple chemical gradients, tend to be more robust
> (less influenced by individual data points).
>
> Use of the lowest response of either survival or growth in the toxicity
> designation framework
> Growth is not independent of survival, so looking at growth by itself
> can be misleading. A number of experts (eg Dave Mount, Chris Ingersoll,
>
> Don MacDonald) are recommending the use of the biomass endpoint (total
> mass of survivors in test sample vs control). The decision to use three
> thresholds based on the lowest of either survival or growth less than
> 70, 80, or 90% of control is highly correlated to the biomass results
> for the HA 28d growth/survival endpoint. [see attached plot showing
> lowest response vs biomass for HA]
> to be continued....
>
> --
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> (See attached file: C_HY28_Biomass.doc)

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